

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 03:55:23 ; Search time 21 Seconds

(without alignments)
308.110 Million cell updates/sec

Title: US-09-867-958-1
Perfect score: 849
Sequence: 1 MARQHARTLYDRPMYFME.....PPAMDDLDSDSADATSN 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	347.5	40.9	160	1	TEBP_HUMAN
2	345.5	40.7	160	1	TEBP_MOUSE
3	311.5	36.7	146	1	TEBP_CHICK
4	125.5	14.6	186	1	WOS2_SCHPO
5	114	13.4	175	1	YOCA_CAEBL
6	99	11.7	215	1	YKLT_YEAST
7	91.5	10.8	704	1	HS85_TRYCR
8	90	10.6	549	1	MIF2_YEAST
9	89.5	10.5	770	1	A4_HUMAN
10	87.5	10.3	751	1	A4_SALSC
11	85.5	10.1	770	1	A4_MOUSE
12	82.5	9.7	611	1	GHR_COILI
13	82	9.7	184	1	YCL17_DROME
14	81	9.5	686	1	YPR4_CAEBL
15	80.5	9.5	703	1	HS83_TRYBB
16	80	9.4	420	1	CAOS_RANES
17	80	9.4	810	1	MCM6_CAEBL
18	79	9.3	770	1	A4_RAT
19	78.5	9.2	517	1	EAS_DROME
20	75.5	8.9	624	1	ATMG_ARXAD
21	75.5	8.9	1192	1	RTM_HUMAN
22	75	8.8	798	1	IC00_MPCPN
23	74.5	8.8	500	1	ANP1_YEAST
24	74.5	8.8	513	1	C4P1_DROME
25	74.5	8.8	590	1	SGR1_SCHPO
26	74.5	8.8	701	1	HS83_LELIN
27	74	8.7	267	1	CGIC_DROME
28	74	8.7	409	1	CAOC_RABIT
29	74	8.7	643	1	YNV4_CAEBL
30	73.5	8.7	630	1	YZ35_METJA
31	72.5	8.5	243	1	GSCB_XENLA
32	72.5	8.5	753	1	ZIN_HUMAN
33	72.5	8.5	1089	1	NMD2_YEAST

34	72	8.5	355	1	ARG3_YEAST
35	72	8.5	388	1	CSP_PLARE
36	72	8.5	406	1	CAOS_CHICK
37	72	8.5	465	1	RN15_HUMAN
38	72	8.5	513	1	RFP_HUMAN
39	71.5	8.4	707	1	ORC1_SCHPO
40	71.5	8.4	1612	1	TP2B_CRILLO
41	71	8.4	439	1	MEAL_HUMAN
42	71	8.4	522	1	RFP_MOUSE
43	70.5	8.3	518	1	NMD3_YEAST
44	70.5	8.3	576	1	YITO_YEAST
45	70.5	8.3	1415	1	ICP4_HSVMG

ALIGNMENTS

RESULT 1
TEBP_HUMAN STANDARD: PRT; 160 AA.
AC Q15185; Q8WU70;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Telomerase-binding protein p23 (Hsp90 co-chaperone) (Progesterone receptor complex p23).
GN TEBP OR P23.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=9415868; PubMed=8114727;
RA Johnson J.L., Belto T.G., Krco C.J., Toft D.O.;
RT "Characterization of a novel 23-kilodalton protein of inactive progesterone receptor complexes.";
RL Mol. Cell. Biol. 14:1956-1963(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Lung, and urinary bladder;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [3]
RP FUNCTION.
RX PubMed=12077419;
RA Freeman B.C., Yamamoto K.R.;
RT "Disassembly of transcriptional regulatory complexes by molecular chaperones.";
RL Science 296:2232-2235(2002).
CC -I- FUNCTION: Molecular chaperone that localizes to genomic response elements in a hormone-dependent manner and disrupts receptor-mediated transcriptional activation, by promoting disassembly of transcriptional regulatory complexes.
CC -I- SUBUNIT: Binds to telomerase and to the progesterone receptor.
CC -I- SIMILARITY: BELONGS TO THE P23 / WOS2 FAMILY.
CC
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CC
CC EMBL: I24804; AAA18537.1; -
CC EMBL: BC003005; AAH03005.1; -
CC EMBL: BC021167; AAH21167.1; -
CC MIM: 607061; -
CC Chapterone.
CC DOMAIN 108 160 ASP/GLU-RICH.
CC SEQUENCE 160 AA; 18697 MW; 235388B9D7AFD73F CRC64;


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OX NCBI_TaxId=4896;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=972;
RA Munoz M., Bejarano E.R., Jimenez J.
RT "The identification of p21wos2, a novel cell cycle regulatory
RT protein which closely interacts with p34cdc2 in the control of the
RT M/G1 transition."
RL Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Wajsbom I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer J., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt K., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880 (2002).
CC -1- FUNCTION: CELL CYCLE REGULATORY PROTEIN THAT INTERACTS WITH CDC2
CC IN THE CONTROL OF THE M-G1 TRANSITION.
CC -1- SIMILARITY: BELONGS TO THE P23 / WOS2 FAMILY.
CC -----
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CC -----
DR EMBL; LA1166; AAA64891.1; -
DR EMBL; Z99262; CAB16411.1; -
KW Cell cycle.
FT DOMAIN 164 186 ASP/GLU-RICH.
FT DOMAIN 170 178 POLY-GLU.
SQ SEQUENCE 186 AA; 20951 MW; 77A3CE60C266265 CRC64;

Query Match 14.8%; Score 125.5; DB 1; Length 186;
Best Local Similarity 25.2%; Pred. No. 7.9e-05;
Matches 32; Conservative 24; Mismatches 52; Indels 19; Gaps 4;

OY 4 QHARTLWYDR-----PMYFMFCVEDSTDVHVLIEDHRIVFSCKNADGVELYNIEF 56
DB 6 OIPEVLMAQORBNKDAEKNAVITYLVLLIPDAVDPKINTLPEKIVDSKSGAANHYAVIDF 65
OY 57 YAKNSKRSQDKRSRST-----CFYRKMKEXVAMPRLTKEDIKPVWLSVDFPNWRDM 110
DB 66 F-----KDIDVSKSYVTGRIYFVLVKKELQEEFWRLTKETKIRLHWLRITDFRWVD- 119
OY 111 EGDDEME 117
DB 120 EDEQDAQ 126

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RESULT 5
YCCA_CAEEL
ID YCCA_CAEEL STANDARD; PRT; 175 AA.
AC Q23280;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 19.4 kDa protein ZC395.10 in chromosome III.
GN ZC395.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=62339;
RN [1]
RP SEQUENCE FROM N.A.
RA Connell M.;
RC STRAIN=Bristol NZ;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE P23 / WOS2 FAMILY.
CC -----
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CC -----
DR EMBL; U13642; AAG00038.1; -
DR WormPep; ZC395.10; CE01436.
KW Hypothetical protein.
FT DOMAIN 145 175 ASP/GLU-RICH.
FT DOMAIN 165 168 POLY-GLU.
SQ SEQUENCE 175 AA; 19431 MW; D5C136F30446E37A CRC64;

Query Match 13.4%; Score 114; DB 1; Length 175;
Best Local Similarity 26.3%; Pred. No. 0.00086;
Matches 31; Conservative 25; Mismatches 58; Indels 4; Gaps 3;

OY 1 MARQIARLWDRPMYFMFCVEDSTDVHVLIEDHRIVFSCKNADGVELYN-EIFYAK 59
DB 1 MAKQ-PTVLMAGRESLVLTVEDEAKIEELKESGNKLFH--QGSSKTDKYATLEFDE 57
OY 60 VNSKRSQDKRSRSTCFYRKMKEXVAMPRLTKEDIKPVWLSVDFPNWRMGDEDEME 117
DB 58 IDPAVKHTGSSSTRVVEITVQKTPAWMPRLQNGNGYHMLKVDGKMKDEDEDEDAE 115

RESULT 6
YKL7_YEAST
ID YKL7_YEAST STANDARD; PRT; 215 AA.
AC P28707;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 24.1 kDa protein in VMA12-APN1 intergenic region.
GN YKL117W OR YKL518.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92221689; PubMed=1561835;
RA Jaquier A., Legrain P., Dujon B.;
RT "Sequence of a 10.7 kb segment of yeast chromosome XI identifies the
RT APN1 and the BAF1 loci and reveals one tRNA gene and several new open
RT reading frames including homologs to RAD2 and Kinases."
RL Yeast 8:121-132(1992).
RN [2]
RP ACETYLATION.

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RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- SIMILARITY: BELONGS TO THE P23 / MOS2 FAMILY.
CC -----
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CC -----
DR EMBL; S93804; AAB2200.1; -;
DR EMBL; Z28117; CAA81957.1; -;
DR PIR; S27382; S27382.
DR SWISS-2DPAGE; P28707; YEAST.
DR SGD; S0001600; YKL117W.
DR Repeat; Acetylation.
KM Repeat; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT REPEAT 140 155 ACETYLATION.
FT REPEAT 159 173
FT DOMAIN 202 212
SQ SEQUENCE 215 AA; 23950 MW; 18859E14429F8DA6 CRC64;

Query Match 11.7%; Score 99; DB 1; Length 215;
Best Local Similarity 27.7%; Pred. No. 0.027;
Matches 23; Conservative 11; Mismatches 19; Indels 30; Gaps 2;

QY 48 VELXNET-----EFYAKVNSKDSQDKRSSRSTICFVRKKMEKAVAPRLRKED 94
DB 68 IDLYKEIIPKTHKAVANGOHYFLKLYKKD-----LESEWPLRLKKEK 110

QY 95 IKPWLVSDFDNMDWEGDEEME 117
DB 111 VKPYPIKTDFDKWDEDEQDEVE 133

RESULT 7
HS85_TRYCR STANDARD; PRT; 704 AA.
ID HS85_TRYCR
AC P06660;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Heat shock like 85 kDa protein.
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_Taxid=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Peru;
RX MEDLINE=87172797; PubMed=3550435;
RA Dragon E.A., Sias S.R., Kato E.A., Gabe J.D.;
RT "The genome of Trypanosoma cruzi contains a constitutively expressed,
RT tandemly arranged multicopy gene homologous to a major heat shock
RT protein.";
RT Mol. Cell. Biol. 7:1271-1275(1987).
RL -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
CC -----
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CC -----
DR EMBL; M15346; AAA30202.1; -;

DR PIR; A26125; A26125.
DR HSP; P07900; 1YER.
DR InterPro; IPR003594; AtPbind_Atpase.
DR InterPro; IPR001404; Hsp90.
DR Pfam; PF00183; Hsp90; 1.
DR Pfam; PF02518; Hsp90; 1.
DR PRINTS; PR00775; HEATSHOCK90.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; PS00298; Hsp90; 1.
DR Chapterone; ATP-binding; Heat shock.
SQ SEQUENCE 704 AA; 80757 MW; EC39D45576FBEA67 CRC64;

Query Match 10.8%; Score 91.5; DB 1; Length 704;
Best Local Similarity 25.6%; Pred. No. 0.54; Indels 17; Gaps 5;
Matches 32; Conservative 22; Mismatches 54;

QY 1 MARQARTLWDRPMYVMEFCVEDSDVHVLIEDHRIVFCCKNADGVE-LYNEIEFYAK 59
DB 191 LIRKHSFIDY-----ILMTVEKATEKEVTDEDEBAATKMEGEPEVVEEKDDAE 244

QY 60 VNSKDSQDKRSSRSTICFVRKKMEKAVAPR---LTKEDIPVWLSVDFNWRMEGDEE 115
DB 245 EGEKKKKKKVKEVTOEFVYQNKHKPLMTBDPKDVTKEVYAFYKAIS---NDWE--EP 298

QY 116 MELAH 120
DB 299 LSTKH 303

RESULT 8
MIF2_YEAST STANDARD; PRT; 549 AA.
ID MIF2_YEAST
AC P35201;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MIF2 protein.
GN MIF2 OR YKL089W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94012984; PubMed=8408221;
RA Brown M.T., Goetsch L., Hartwell L.H.;
RT "MIF2 is required for mitotic spindle integrity during anaphase
RT spindle elongation in Saccharomyces cerevisiae.";
RT J. Cell Biol. 123:387-403(1993).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RA Pohl T.M., Pohl F.M.;
RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=96086494; PubMed=7579695;
RA Meluh P.B., Koshland D.;
RT "Evidence that the MIF2 gene of Saccharomyces cerevisiae encodes a
RT centromere protein with homology to the mammalian centromere protein
RT CENP-C.";
RT Mol. Biol. Cell 6:793-807(1995).
RL -1- FUNCTION: REQUIRED FOR MITOTIC SPINDLE INTEGRITY DURING ANAPHASE
CC SPINDLE ELONGATION. PROBABLY BINDS AT TRACTS IN DNA. INTERACTS
CC WITH CEP1.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; CENTROMERIC.
CC -1- SIMILARITY: SOME, TO MAMMALIAN CENP-C.
CC -----
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CC      -----
CC      EMBL: Z18294; CAA79163.1;
CC      EMBL: Z28089; CAA81927.1;
CC      PIR: S37914; S37914.
CC      SGD: S0001572; MTF2.
CC      InterPro: IPR00637; AT_hook.
CC      Pfam: PF02178; AT_hook.1.
CC      SMART: SM00384; AT_hook.1.
CC      Mitosis; Nuclear protein; DNA-binding; Repeat; Centromere;
CC      Phosphorylation.
CC      DOMAIN 178 263 ASP/GLU-RICH (ACIDIC).
CC      DNA_BIND 356 364 A.T HOOK (POTENTIAL).
CC      MOD_RES 325 325 PHOSPHORYLATION (BY SIMILARITY).
CC      MOD_RES 387 387 PHOSPHORYLATION (BY SIMILARITY).
CC      SEQUENCE 549 AA; 62472 MW; A6A4FAC9F6B6EB1 CRC64;

Query Match 10.6%; Score 90; DB 1; Length 549;
Best Local Similarity 21.8%; Pred No. 0.56;
Matches 26; Conservative 26; Mismatches 39; Indels 28; Gaps 3;

QY 41 SCKNADGVELYNEIFYAFVNSKDSOD-----KRSRSITCEV 78
DB 236 SASDSDGDTYQVEBEAEAVNTNEDDYIRQASDVFTDSLDRNGLRKSTRVAVDL 295
QY 79 KKKK-EKXAMPRLTKEDIPVLSVDFDWMRMGEDEEMLAHVEHYAELKKVSTKRP 136
DB 296 QYMRKEKTYKKRSKPKVLDIKIYTYD-----ESEDEEELIAAQRRKKOKKKKPTPTRP 349

RESULT 9
AA_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE (PN-II) (APP1) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI-Taxid-9606;
RX MEDLINE-871144572; PubMed-2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor."
RT Nature 325:733-736(1987).
RN [12]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-88122639; PubMed-2893289;
RA Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors."
RT Nature 331:525-527(1988).
RN [13]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-89128427; PubMed-2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The Phe4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons."
RN [14]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-97263807; PubMed-9108164;
RA Hattori M., Tsukahara F., Furubata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus."
RT Nucleic Acids Res. 25:1802-1808(1997).
RN [15]
RN RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE-88122640; PubMed-2893290;
RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease."
RT Nature 331:528-530(1988).
RN [16]
RN RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE-88122641; PubMed-2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity."
RT Nature 331:530-532(1988).
RN [17]
RN RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE-87231971; PubMed-3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides."
RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [18]
RN RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE-88124854; PubMed-2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex."
RT Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RN RP SEQUENCE OF 672-681.
RX MEDLINE-88035004; PubMed-3312495;
RA Pardinge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtelotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiotensin of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels."
RT J. Neurochem. 49:1394-1401(1987).
RN [110]
RN RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE-90236318; PubMed-2110105;
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene."
RT Gene 87:257-263(1990).
RN [111]
RN RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE-89016647; PubMed-3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide."
RT Nucleic Acids Res. 16:9351-9351(1988).
RN [112]
RN RP SEQUENCE OF 18-50.
RX MEDLINE-87250462; PubMed-3597385;
RA Van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts."
RT J. Biol. Chem. 262:8508-8514(1987).
RN [113]
RN RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE-89384866; PubMed-2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with

```

RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RA MEDLINE-90211252; PubMed-1969731;
 RX Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RA MEDLINE-93188965; PubMed-8446172;
 RX Nishimuro I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 protein G(O)."
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RA MEDLINE-99215582; PubMed-10201399;
 RX Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaupt G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RA MEDLINE-91104913; PubMed-125487;
 RX Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RA MEDLINE-92031488; PubMed-1718421;
 RX Heald S.L., Tilton R.F., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamack M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburlini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RA MEDLINE-94281210; PubMed-7516706;
 RX Talaious J., Marchowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RA MEDLINE-97128622; PubMed-8973180;
 RX Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RA MEDLINE-98359783; PubMed-9693002;
 RX Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-mimicelle
 environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RA MEDLINE-20400066; PubMed-10940222;
 RX Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.

RX MEDLINE-20400065; PubMed-10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RA MEDLINE-88296437; PubMed-2900137;
 RX Dyrks T., Weidemann A., Multhaupt G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 amyloid A precursor of Alzheimer's disease.";
 CC Query Match 10.5%; Score 89.5; DB 1; Length 770;
 CC Best Local Similarity 22.2%; Pred. No. 0.92;
 CC Matches 30; Conservative 25; Mismatches 43; Indels 37; Gaps 4;
 OY 17 VFMECVDSIDVHVLIEDHRIYFCKNADGVETLNEIFYAKVNSKDSQRRSRITC 76
 DB 153 VAKETCSKSTNLH---DYGMLPC---GIDKRGVEYVCCPLAESDNVDSADA--- 201
 OY 77 FVRKWEKRVAMPRLTKEDIKPVWLSDPDNMRDMEGDEMELEAHVHYAELLKVSTKRP 136
 DB 202 -----EEDSDVWVGADPTDYADGSEDKVVEAEDEEVAEE----- 239
 OY 137 PPAMDLDSDSDAD 151
 DB 240 ---EADDDDEDED 250
 RESULT 10
 A4_SAIISC STANDARD; PRT; 751 AA.
 AC 095241;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
 amyloid protein (Beta-Ap4) (A-beta)].
 GN App.
 OS Saimiri sciureus (Common squirrel monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE-96108492; PubMed-8532114;
 RA Levy E., Amornin A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 G(O).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 NKXV MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BP1/KUNITZ INHIBITOR DOMAIN.
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 or send an email to license@sdb-sib.ch).

DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOID4.
 DR PRINTS: PR00759; BASICTPASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT CARBOHYD 289 289
 FT VARSPLIC 290 364
 FT VARSPLIC 346 380
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

Query Match 10.1%; Score 85.5; DB 1; Length 770;
 Best Local Similarity 22.1%; Pred. No. 2.2;
 Matches 31; Conservative 22; Mismatches 40; Indels 47; Gaps 5;

QY 17 VMEFEVSTDVHVLIEDHRIIVSCKNADGVELYNEIEFYA-----KVNKSQDSQKRSS 71
 DB 153 VAKETCESEKSTNLH-----DYGMLLPCC-----GIDKRGVEFYCCPLAESDSVDSAD----- 200
 QY 72 RSTICEFRKKMEKVAAPRLFKEDIKPVWLSDVDFNMRWMEDEMELAHVEHYAELKKV 131
 DB 201 -----AEEDSDVWVGADTDYADGSDKVAEEAEVEADVEE-- 239
 QY 132 STRKPPAMDLDLDDSDAD 151
 DB 240 -----EADDEDEVED 250

RESULT 12
 ID GHR_COLL1 STANDARD; PRT; 611 AA.
 AC 090375;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
 GN GHR.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 OX NCBI_Taxid=9932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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DR EMBL: U20353; AAA84745.1; -
 DR HSP: P10912; IAXI.
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hemtopoptn_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 611
 FT DOMAIN 21 240
 FT TRANSMEM 241 264
 FT DOMAIN 265 611
 FT DOMAIN 119 226
 FT DISULFID 34 44
 FT DISULFID 75 86
 FT DISULFID 100 114
 FT CARBOHYD 16 16
 FT CARBOHYD 53 53
 FT CARBOHYD 89 89
 FT CARBOHYD 130 130
 FT CARBOHYD 135 135
 FT CARBOHYD 174 174
 SQ SEQUENCE 611 AA; 68851 MW; CA8750BF9EAE1BDA CRC64;

Query Match 9.7%; Score 82.5; DB 1; Length 611;
 Best Local Similarity 21.4%; Pred. No. 3.1;
 Matches 39; Conservative 23; Mismatches 53; Indels 67; Gaps 7;

QY 7 RFLWDRPMYV-FMEFEVSTDVHVLIEDHRIIVSCKN----- 45
 DB 309 KTLQNDLWVEFLIEDPEDEKRVSDTD-RILSEHLKSHSLGAKDDSGRASCE 367
 QY 46 -----DGYELNYEIEFYAKVNKSQDSQKRSSITCEVKKMEKVAAPRLFKED 94
 DB 368 PDIPETDSASDFCDALSDIDQFKVTEKE-----EDLICLRKDNDE-SLPSLAWTD 419
 QY 95 IKPVWLSDVDFNMRWMEDEMELAHVEHYAELKKVSTRKPPAMDLDLDDSDADAT 154
 DB 420 TQQPRMSTRPENSQPW-----PPPADSIDAASPSAHNOL 453
 QY 155 SN 156
 DB 454 SN 455

RESULT 13
 ID YC17_DROME STANDARD; PRT; 184 AA.
 AC 09YH95;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein CG16817.
 GN CG16817
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]


```

RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Cealinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Abril J.F., Abdayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brokstein P., Bottler P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler E., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yeo Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE P23 / MOS2 FAMILY.
CC -----
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CC -----
DR EMBL: AE003683; AAF54424.1; -
DR Flybase: FBgn0037728; CG16817.
KM Hypothetical protein.
FT DOMAIN
FT 145
FT 184
SQ SEQUENCE 184 AA; 20753 MW; 982909B6B255DB08 CRC64;

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RESULT 14
ID YPR4_CAEEL STANDARD; PRT; 686 AA.
AC 020059;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Hypothetical 77.0 kDa Trp-Asp repeats containing protein F35G12.4 in
DE chromosome III.
GN F35G12.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
ON NCBI_TaxID=6239;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Guai C.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
DR EMBL: Z46242; CAA86335.1; -
DR Wormpep: F35G12.4; CE03286.
DR Interpro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 6.
DR PRINTS: PR00320; GPROTEINRPT.
DR PRODOM: PD000018; WD40; 2.
DR SMART: SM00320; WD40; 6.
DR PROSITE: PS00678; WD_REPEATS_1; 2.
DR PROSITE: PS00678; WD_REPEATS_2; 4.
DR PROSITE: PS00678; WD_REPEATS_3; 4.
DR PROSITE: PS00678; WD_REPEATS_4; 1.
KM Hypothetical protein; Repeat; WD repeat.
FT REPEAT
FT 27
FT REPEAT
FT 88
FT REPEAT
FT 133
FT REPEAT
FT 176
FT REPEAT
FT 218
FT REPEAT
FT 260
FT REPEAT
SQ SEQUENCE 686 AA; 77014 MW; D2946473DA2843BD CRC64;

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Query Match 9.7%; Score 82; DB 1; Length 184;
Best Local Similarity 20.0%; Pred. No. 0.84;
Matches 29; Conservative 25; Mismatches 63; Indels 28; Gaps 4;

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Query Match 9.5%; Score 81; DB 1; Length 686;
Best Local Similarity 24.6%; Pred. No. 4.9;
Matches 35; Conservative 31; Mismatches 52; Indels 24; Gaps 9;

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DE Heat shock protein 83.
GN HSP83.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=LESTER SERODME;
RX MEDLINE=90136708; PubMed=2515434;
RA Mottam J., Murphy W., Agabian N.;
RT "A transcriptional analysis of the Trypanosoma brucei hsp83 gene
   cluster";
RL Mol. Biochem. Parasitol. 37:115-128(1989).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
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CC -----
DR EMBL; X14176; CAA32377.1; -.
DR PIR; S08119; S08119.
DR HSSP; P07900; 1YER.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001404; Hsp90.
DR Pfam; PF00183; HSP90; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00775; HEATSHOCK90.
DR SMART; SM00387; HATPase_c; 1.
DR PROSITE; PS00298; HSP90; 1.
DR KW Chaperone: ATP-binding; Heat shock.
SQ SEQUENCE 703 AA; 80715 MW; 50D7BB33A303B70 CRC64;

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Query Match          9.5%; Score 80.5; DB 1; Length 703;
Best Local Similarity 24.0%; Pred. No. 5.7;
Matches 30; Conservative 25; Mismatches 53; Indels 17; Gaps 5;

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QY 1 MARQHARTIMYDRPMYVMEFCVEDSTVHYVLIEDRIYFSCKNADGYE-LYNEIEFYAK 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 LIKHSEFIDG-----IELMVENTTEKEYTDEDEDEBAKKAEGEPKVEYKGDVD 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 VNSKDSODKRSRSITCFVRKKEKVAMP---LTKEIDIKPVWLSVDFDWMRDWEGDEE 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 245 ADAKKKKTKKYEKQEFVONKHKPLMTROPKDYTKKEEYASFYKAIS---NDWE--EQ 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 MELAH 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 LSTKH 303

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Search completed: March 20, 2003, 05:18:37
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